

ENTERED

RAW SEQUENCE LISTING

DATE: 04/18/2002 PS

TIME: 11:06:15

PATENT APPLICATION: US/10/044,303

Input Set : A:\Vectorsl.app

Output Set: N:\CRF3\04182002\J044303.raw

```
3 <110> APPLICANT: Max-Planck-Gesellschaft e.V.
      5 <120> TITLE OF INVENTION: Protein expression and structure solution using
              specific fusion vectors
      8 <130> FILE REFERENCE: ST010209-EPA
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/044,303
C--> 11 <141> CURRENT FILING DATE: 2002-01-11
     13 <160> NUMBER OF SEQ ID NOS: 3
     15 <170> SOFTWARE: PatentIn Ver. 2.1
    17 <210> SEQ ID NO: 1
    18 <211> LENGTH: 765
    19 <212> TYPE: PRT
    20 <213> ORGANISM: Artificial Sequence
    22 <220> FEATURE:
    23 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial myosin
             sequence of Dictyostelium; Component (1) of the
    25
             recombinant protein M761-2R R238E
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    31 Lys Tyr Leu Lys Val Lys Gln Gly Asp Ser Asp Leu Phe Lys Leu Thr
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    34 Val Ser Asp Lys Arg Tyr Ile Trp Tyr Asn Pro Asp Pro Lys Glu Arg
                                    40
    37 Asp Ser Tyr Glu Cys Gly Glu Ile Val Ser Glu Thr Ser Asp Ser Phe
    40 Thr Phe Lys Thr Val Asp Gly Gln Asp Arg Gln Val Lys Lys Asp Asp
                            70
    43 Ala Asn Gln Arg Asn Pro Ile Lys Phe Asp Gly Val Glu Asp Met Ser
    46 Glu Leu Ser Tyr Leu Asn Glu Pro Ala Val Phe His Asn Leu Arg Val
    47
                   100
                                       105
    49 Arg Tyr Asn Gln Asp Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Leu Val
                                   120
    52 Ala Val Asn Pro Phe Lys Arg Ile Pro Ile Tyr Thr Gln Glu Met Val
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                                                   140
    55 Asp Ile Phe Lys Gly Arg Arg Asn Glu Val Ala Pro His Ile Phe
                           150
                                               155
    58 Ala Ile Ser Asp Val Ala Tyr Arg Ser Met Leu Asp Asp Arg Gln Asn
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                                           170
   61 Gln Ser Leu Leu Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn
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                                       185
   64 Thr Lys Lys Val Ile Gln Tyr Leu Ala Ser Val Ala Gly Arg Asn Gln
              195
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205

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67 68	Ala	Asn 210	Gly	Ser	Gly	Val	Leu 215	Glu	Gln	Gln	Ile	Leu 220	Gln	Ala	Asn	Pro
70 71	Ile 225	Leu	Glu	Ala	Phe	Gly 230		Ala	Lys	Thr	Thr 235	Arg	Asn	Asn	Asn	
		Arg	Phe	Gly	Lys 245		Ile	Glu	Ile		Phe	Asn	Ser	Ala	Gly	240 Phe
	Ile	Ser	Gly	Ala 260		Ile	Gln	Ser	Tyr	250 Leu	Leu	Glu	Lys		255 Arg	Val
79	Val	Phe	Gln		Glu	Thr	Glu	Arg	265 Asn	Tyr	His	Ile	Phe	270 Tyr	Gln	Leu
80 82	Leu	Ala	275 Gly	Ala	Thr	Ala	Glu	280 Glu	Lys	Lys	Ala	Leu	285 His	Leu	Ala	Glv
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91 92	Ile	Val	Gly	Phe 340	Ser	Gln	Glu	Glu	Gln 345		Ser	Ile	Phe		Ile	Ile
94	Ala	Glv	Tle	_	Hic	Τ.Δ11	C1v	λen		Tira	Dha	a1	T	350	Ala	
95			355					360					365			
98		3/0					375					380			Ser	
100	Val	Phe	Gly	Val	Asn	Pro	Ser	Val	Leu	Glu	Lys	Ala	Leu	Met	Glu	Pro
TOT	383					390					395					400
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106 107 109	Lys		Leu	Ser 420 Trp	405 Ser	Arg	Asp	Ala Lys	Leu 425	410 Val	Lys	Ala	Leu Leu	Tyr 430	415 Gly	Arg
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106 107 109 110 112	Lys Leu	Phe Lys	Leu 435	Ser 420 Trp	405 Ser Leu	Arg Val	Asp Lys Gly	Ala Lys 440	Leu 425 Ile	410 Val Asn	Lys Asn	Ala Val Ser	Leu Leu 445	Tyr 430 Cys	415 Gly	Arg Glu
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106 107 109 110 112 113 115	Lys Leu Arg	Phe Lys 450	Leu 435 Ala	Ser 420 Trp	405 Ser Leu Phe	Arg Val Ile Phe	Asp Lys Gly 455	Ala Lys 440 Val	Leu 425 Ile Leu	410 Val Asn Asp	Lys Asn Ile	Ala Val Ser	Leu Leu 445 Gly	Tyr 430 Cys Phe	415 Gly Gln	Arg Glu Ile Glu
106 107 109 110 112 113 115 116	Lys Leu Arg Phe 465	Phe Lys 450 Lys	Leu 435 Ala Val	Ser 420 Trp Tyr Asn	405 Ser Leu Phe Ser	Arg Val Ile Phe 470	Asp Lys Gly 455 Glu	Ala Lys 440 Val Gln	Leu 425 Ile Leu Leu	410 Val Asn Asp Cys	Lys Asn Ile Ile 475	Ala Val Ser 460 Asn	Leu Leu 445 Gly Tyr	Tyr 430 Cys Phe	415 Gly Gln Glu Asn	Arg Glu Ile Glu
106 107 109 110 112 113 115 116	Lys Leu Arg Phe 465	Phe Lys 450 Lys	Leu 435 Ala Val	Ser 420 Trp Tyr Asn	405 Ser Leu Phe Ser	Arg Val Ile Phe 470	Asp Lys Gly 455 Glu	Ala Lys 440 Val Gln	Leu 425 Ile Leu Leu	410 Val Asn Asp Cys Met	Lys Asn Ile Ile 475	Ala Val Ser 460 Asn	Leu Leu 445 Gly Tyr	Tyr 430 Cys Phe	415 Gly Gln Glu Asn Gln	Arg Glu Ile Glu
106 107 109 110 112 113 115 116 118	Lys Leu Arg Phe 465 Lys	Phe Lys 450 Lys Leu	Leu 435 Ala Val Gln	Ser 420 Trp Tyr Asn Gln	405 Ser Leu Phe Ser Phe 485	Arg Val Ile Phe 470 Phe	Asp Lys Gly 455 Glu Asn	Ala Lys 440 Val Gln His	Leu 425 Ile Leu Leu	410 Val Asn Asp Cys Met 490	Lys Asn Ile Ile 475 Phe	Ala Val Ser 460 Asn Lys	Leu Leu 445 Gly Tyr Leu	Tyr 430 Cys Phe Thr	415 Gly Gln Glu Asn Gln	Arg Glu Ile Glu 480 Glu
106 107 109 110 112 113 115 116 118 119 121 122	Lys Leu Arg Phe 465 Lys Glu	Phe Lys 450 Lys Leu Tyr	Leu 435 Ala Val Gln Leu	Ser 420 Trp Tyr Asn Gln Lys 500	A05 Ser Leu Phe Ser Phe 485 Glu	Arg Val Ile Phe 470 Phe Lys	Asp Lys Gly 455 Glu Asn Ile	Ala Lys 440 Val Gln His	Leu 425 Ile Leu His Trp 505	Asn Asp Cys Met 490 Thr	Lys Asn Ile Ile 475 Phe	Ala Val Ser 460 Asn Lys Ile	Leu 445 Gly Tyr Leu Asp	Tyr 430 Cys Phe Thr Glu Phe	Gly Glu Asn Gln 495 Gly	Arg Glu Ile Glu 480 Glu Leu
106 107 109 110 112 113 115 116 118 119 121 122 124	Lys Leu Arg Phe 465 Lys Glu Asp	Phe Lys 450 Lys Leu Tyr	Leu 435 Ala Val Gln Leu Gln	Ser 420 Trp Tyr Asn Gln Lys 500 Ala	A05 Ser Leu Phe Ser Phe 485 Glu	Arg Val Ile Phe 470 Phe Lys	Asp Lys Gly 455 Glu Asn Ile	Ala Lys 440 Val Gln His	Leu 425 Ile Leu His Trp 505	Asn Asp Cys Met 490 Thr	Lys Asn Ile Ile 475 Phe	Ala Val Ser 460 Asn Lys Ile	Leu 445 Gly Tyr Leu Asp	Tyr 430 Cys Phe Thr Glu Phe	Gly Glu Asn Gln 495 Gly	Arg Glu Ile Glu 480 Glu Leu
106 107 109 110 112 113 115 116 118 119 121 122 124 125	Lys Leu Arg Phe 465 Lys Glu Asp	Phe Lys 450 Lys Leu Tyr	Leu 435 Ala Val Gln Leu Gln 515	Ser 420 Trp Tyr Asn Gln Lys 500 Ala	Leu Phe Ser Phe 485 Glu Thr	Arg Val Ile Phe 470 Phe Lys Ile	Asp Lys Gly 455 Glu Asn Ile Asp	Ala Lys 440 Val Gln His Asn Leu 520	Leu 425 Ile Leu His Trp 505 Ile	Asn Asp Cys Met 490 Thr	Lys Asn Ile Ile 475 Phe Phe Gly	Ala Val Ser 460 Asn Lys Ile Arg	Leu 445 Gly Tyr Leu Asp Gln 525	Tyr 430 Cys Phe Thr Glu Phe 510 Pro	Glu Asn Gln 495 Gly	Arg Glu Ile Glu 480 Glu Leu Gly
106 107 109 110 112 113 115 116 118 119 121 122 124 125 127	Lys Leu Arg Phe 465 Lys Glu Asp	Phe Lys 450 Lys Leu Tyr Ser Leu	Leu 435 Ala Val Gln Leu Gln 515	Ser 420 Trp Tyr Asn Gln Lys 500 Ala	Leu Phe Ser Phe 485 Glu Thr	Arg Val Ile Phe 470 Phe Lys Ile	Asp Lys Gly 455 Glu Asn Ile Asp Glu	Ala Lys 440 Val Gln His Asn Leu 520	Leu 425 Ile Leu His Trp 505 Ile	Asn Asp Cys Met 490 Thr	Lys Asn Ile Ile 475 Phe Phe Gly	Ala Val Ser 460 Asn Lys Ile Arg	Leu 445 Gly Tyr Leu Asp Gln 525	Tyr 430 Cys Phe Thr Glu Phe 510 Pro	Glu Asn Gln 495 Gly	Arg Glu Ile Glu 480 Glu Leu Gly
106 107 109 110 112 113 115 116 118 119 121 122 124 125 127 128	Lys Leu Arg Phe 465 Lys Glu Asp Ile	Phe Lys 450 Lys Leu Tyr Ser Leu 530	Leu 435 Ala Val Gln Leu Gln 515 Ala	Ser 420 Trp Tyr Asn Gln Lys 500 Ala Leu	Leu Phe Ser Phe 485 Glu Thr Leu	Arg Val Ile Phe 470 Phe Lys Ile Asp	Asp Lys Gly 455 Glu Asn Ile Asp Glu 535	Ala Lys 440 Val Gln His Asn Leu 520 Gln	Leu 425 Ile Leu His Trp 505 Ile Ser	Asn Asp Cys Met 490 Thr Asp Val	Lys Asn Ile Ile 475 Phe Phe Gly Phe	Ala Val Ser 460 Asn Lys Ile Arg Pro 540	Leu 445 Gly Tyr Leu Asp Gln 525 Asn	Tyr 430 Cys Phe Thr Glu Phe 510 Pro	Gln Glu Asn Gln 495 Gly Pro	Arg Glu Ile Glu 480 Glu Leu Gly Asp
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106 107 109 110 112 113 115 116 118 119 121 122 124 125 127 128 130 131	Lys Leu Arg Phe 465 Lys Glu Asp Ile Asn 545	Phe Lys 450 Lys Leu Tyr Ser Leu 530 Thr	Leu 435 Ala Val Gln Leu Gln 515 Ala	Ser 420 Trp Tyr Asn Gln Lys 500 Ala Leu Ile	A05 Ser Leu Phe Ser Phe 485 Glu Thr Leu Thr	Arg Val Ile Phe 470 Phe Lys Ile Asp Lys 550	Asp Gly 455 Glu Asn Ile Asp Glu 535 Leu	Ala Lys 440 Val Gln His Asn Leu 520 Gln His	Leu 425 Ile Leu His Trp 505 Ile Ser	Asn Asp Cys Met 490 Thr Asp Val	Lys Asn Ile Ile 475 Phe Gly Phe Phe 555	Ala Val Ser 460 Asn Lys Ile Arg Pro 540 Ser	Leu 445 Gly Tyr Leu Asp Gln 525 Asn	Tyr 430 Cys Phe Thr Glu Phe 510 Pro Ala	Gln Glu Asn Gln 495 Gly Pro Thr	Arg Glu Ile Glu 480 Glu Leu Gly Asp
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 106 107 109 110 112 113 115 116 118 119 121 122 124 125 127 128 130 131 133 134	Lys Leu Arg Phe 465 Lys Glu Asp Ile Asn 545 Lys	Phe Lys 450 Lys Leu Tyr Ser Leu 530 Thr	Leu 435 Ala Val Gln Leu Gln 515 Ala Leu	Ser 420 Trp Tyr Asn Gln Lys 500 Ala Leu Ile Glu	A05 Ser Leu Phe Ser Phe 485 Glu Thr Leu Thr Pro 565	Arg Val Ile Phe 470 Phe Lys Ile Asp Lys 550 Arg	Asp Lys Gly 455 Glu Asn Ile Asp Glu 535 Leu Phe	Ala Lys 440 Val Gln His Asn Leu 520 Gln His Ser	Leu 425 Ile Leu His Trp 505 Ile Ser Ser Lys Ile	Asn Asp Cys Met 490 Thr Asp Val His Thr 570	Lys Asn Ile Ile 475 Phe Gly Phe Phe 555 Glu	Ala Val Ser 460 Asn Lys Ile Arg Pro 540 Ser Phe	Leu 445 Gly Tyr Leu Asp Gln 525 Asn Lys Gly	Tyr 430 Cys Phe Thr Glu Phe 510 Pro Ala Lys Val Glu	Glu Asn Gln 495 Gly Pro Thr Asn	Arg Glu Ile Glu 480 Glu Leu Gly Asp Ala 560 His
 106 107 109 110 112 113 115 116 118 119 121 122 124 125 127 128 130 131 133 134 136 137	Lys Leu Arg Phe 465 Lys Glu Asp Ile Asn 545 Lys Tyr	Phe Lys 450 Lys Leu Tyr Ser Leu 530 Thr Tyr	Leu 435 Ala Val Gln Leu Gln 515 Ala Leu Glu Gly	Ser 420 Trp Tyr Asn Gln Lys 500 Ala Leu Ile Glu Gln 580	A05 Ser Leu Phe Ser Phe 485 Glu Thr Leu Thr Pro 565 Val	Arg Val Ile Phe 470 Phe Lys Ile Asp Lys 550 Arg Met	Asp Lys Gly 455 Glu Asn Ile Asp Glu 535 Leu Phe Tyr	Ala Lys 440 Val Gln His Asn Leu 520 Gln His Ser	Leu 425 Ile Leu His Trp 505 Ile Ser Ser Lys Ile 585	Asn Asp Cys Met 490 Thr Asp Val His Thr 570 Gln	Lys Asn Ile Ile 475 Phe Phe Gly Phe Phe 555 Glu Asp	Ala Val Ser 460 Asn Lys Ile Arg Pro 540 Ser Phe Trp	Leu 445 Gly Tyr Leu Asp Gln 525 Asn Lys Gly Leu	Tyr 430 Cys Phe Thr Glu Phe 510 Pro Ala Lys Val	Gln Glu Asn Gln 495 Gly Pro Thr Asn Thr	Arg Glu Ile Glu 480 Glu Leu Gly Asp Ala 560 His

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                             615
 145 Ala Lys Lys Gly Ala Asn Phe Ile Thr Val Ala Ala Gln Tyr Lys Glu
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 148 Gln Leu Ala Ser Leu Met Ala Thr Leu Glu Thr Thr Asn Pro His Phe
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                                         650
151 Val Arg Cys Ile Ile Pro Asn Asn Lys Gln Leu Pro Ala Lys Leu Glu
152
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154 Asp Lys Val Val Leu Asp Gln Leu Arg Cys Asn Gly Val Leu Glu Gly
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            675
                                 680
157 Ile Arg Ile Thr Arg Lys Gly Phe Pro Asn Arg Ile Ile Tyr Ala Asp
                            695
                                                 700
160 Phe Val Lys Arg Tyr Tyr Leu Leu Ala Pro Asn Val Pro Arg Asp Ala
                        710
                                             715
163 Glu Asp Ser Gln Lys Ala Thr Asp Ala Val Leu Lys His Leu Asn Ile
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                                         730
166 Asp Pro Glu Gln Tyr Arg Phe Gly Ile Thr Lys Ile Phe Phe Arg Ala
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                740
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169 Gly Gln Leu Ala Arg Ile Glu Glu Ala Arg Glu Gln Arg
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175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial Sequence
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179 <223> OTHER INFORMATION: Description of Artificial Sequence: Whole sequence
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182 <220> FEATURE:
183 <223> OTHER INFORMATION: The protein comprises as component (1) the aa
184
          sequence of myosin II motor domain of
185
         Dictyostelium, a three aa linker region and the
          a-actinin aa sequence
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            35
198 Asp Ser Tyr Glu Cys Gly Glu Ile Val Ser Glu Thr Ser Asp Ser Phe
                             55
201 Thr Phe Lys Thr Val Asp Gly Gln Asp Arg Gln Val Lys Lys Asp Asp
202
                                             75
204 Ala Asn Gln Arg Asn Pro Ile Lys Phe Asp Gly Val Glu Asp Met Ser
205
                     85
                                         90
207 Glu Leu Ser Tyr Leu Asn Glu Pro Ala Val Phe His Asn Leu Arg Val
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                                    105
210 Arg Tyr Asn Gln Asp Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Leu Val
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			ASII	PLO	Pne	гаг		TTE	PIO	TTE	тут		GIII	GIU	Met	Val
214		130	-1	_	0.1		135			a 1	77- 1	140	D	***	- 1 -	Dh -
	_	TTE	Phe	Lys	GIY	_	Arg	Arg	Asn	GIU		Ата	Pro	HIS	Ile	
	145					150					155					160
219	Ala	Ile	Ser	Asp		Ala	Tyr	Arg			Leu	Asp	Asp	Arg	Gln	Asn
220					165					170					175	
222	Gln	Ser	Leu	Leu	Ile	Thr	Gly	Glu	Ser	Gly	Ala	Gly	Lys	Thr	Glu	Asn
223				180					185					190		
225	Thr	Lys	Lys	Val	Ile	Gln	Tyr	Leu	Ala	Ser	Val	Ala	Gly	Arg	Asn	Gln
226			195					200					205			
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231	Ile	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Thr	Arq	Asn	Asn	Asn	Ser
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		Arσ	Phe	Glv	Lvs		Ile	Glu	Ile	Gln	Phe	Asn	Ser	Ala	Gly	Phe
235	001			<u>1</u>	245					250					255	
	τlם	Car	Glv	Δla		Tle	Gln	Ser	Tur		Len	Glu	Lvs	Ser	Arg	Va l
238	110	SCI	OLY	260	OCI	110	OIII	DCL	265	ЦСИ	LCu	0±u		270	9	, 41
	T/a l	Dho	Cln		G1u	Thr	Glu	λrα		Ψτεν	Hic	ΤlΔ	Dho		Gln	T.Ou
		FILE	275	Set	Giu	1111	GIU	280	USII	ıyı	шъ	110	285	1 Y L	GIII	пец
241		31-		7 1 n	mba	77.	<i>a</i> 1		T ***	T ***	7 l n	LOU	_	Tou	7 15	C1.
			GTĀ	Ald	TILL	Ата		GIU	гуѕ	гуу	Ата		птъ	ьeu	Ala	GIY
244		290				_	295		a 1	0	a1	300	77 - 1	3	T1 =	T
		GIu	ser	Pne	Asn		ьeu	Asn	GIN	ser		Cys	vaı	Asp	Ile	
	305	_				310			_		315	_				320
	GIY	Val	Ser	Asp		Glu	GIu	Phe	Lys		Thr	Arg	GIn	Ala	Met	Asp
250		_	_		325					330	_		_•	_	335	
	Ile	Val	Gly		Ser	Gln	Glu	Glu		Met	Ser	Ile	Phe		Ile	Ile
253				340					345					350		
255	Ala	Gly	Ile	Leu	His	Leu	Gly	Asn	Ile	Lys	Phe	Glu	Lys	Gly	Ala	Gly
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258	Glu	Gly	Ala	Val	Leu	Lys	Asp	Lys	Thr	Ala	Leu	Asn	Ala	Ala	Ser	Thr
259		370					375					380				
261	Val	Phe	Gly	Val	Asn	Pro	Ser	Val	Leu	Glu	Lys	Ala	Leu	Met	Glu	Pro
262	385					390					395					400
264	Arg	Ile	Leu	Ala	Gly	Arg	Asp	Leu	Val	Ala	Gln	His	Leu	Asn	Val	Glu
265					405					410					415	
267	Lys	Ser	Ser	Ser	Ser	Arq	Asp	Ala	Leu	Val	Lys	Ala	Leu	Tyr	Gly	Arg
	•						-							430		_
270	Leu	Phe	Leu	grT	Leu	Val	Lvs	Lvs	Ile	Asn	Asn	Val	Leu		Gln	Glu
271			435				-1-	440					445	-		
	Ara	Lvs		Tvr	Phe	Tle	G1v		Len	Asp	Tle	Ser		Phe	Glu	Tle
274	*** 9	450		~ 1 *			455			r		460	1			
	Dhe		Val	Δan	Ser	Phe		Gln	Len	Cvs	Tle		Tvr	Thr	Asn	Glu
	465	пуз	vu.	LOII	DGI	470	JIU	U 111	LCu	C13	475	-1011	+1+			480
		Lou	Cln	Cln	Dho		λαη	Uie	uie	Mot		Lve	Leu	Glu	Gln	
280	пур	ьeu	GTII	GIII	485	LIIG	UDII	птэ	HTS	490	1116	пÃЭ	шeu	GIU	495	JIU
	c1	m	T 633	T		T ***	T1~	7 0 0	TI rr		Dha	т1 с	λαν	Dho	Gly	Lou
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283				500					505					510		

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285 286		Ser	Gln 515		Thr	Ile	Asp	Leu 520		Asp	Gly	Arg	Gln 525		Pro	Gly
		T OU			Τ ου	N a m	<i>c</i> 1			. 17-7	Dh.	D			m l.	_
				Leu	Leu	ASP			ser	val	Pne			Ala	Thr	Asp
289		530			1	_	535		_	•		540				
			ren	шe	Thr			His	Ser	His			Lys	Lys	Asn	Ala
	545					550					555					560
294	Lys	Tyr	Glu	Glu	Pro	Arg	Phe	Ser	Lys	Thr	Glu	Phe	Gly	Val	Thr	His
295	i				565					570					575	
297	Tyr	Ala	Gly	Gln	Val	Męt	Tyr	Glu	Ile	Gln	Asp	Trp	Leu	Glu	Lvs	Asn
298				580			_		585		-	-		590	_	
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301		-	595					600			-1-		605		501	
		Asn			Thr	T.ve	Τ.Δ.1			Acn	Dro	A cn		7 l n	Cor	7 ~~
304		610	, 41			2,5	615		ASII	nsp	110	620	TTE	ALG	Set	Arg
			Two	C1**	Ala	A an			шhъ	17.0 1	71-		01 =	m	.	01
			гуз	GIY	ніа		Pile	TIE	THE	val		Ата	GIN	туг	гàг	
	625			_	_	630			_		635	_				640
		Leu	Ala	Ser	Leu	Met	Ala	Thr	Leu		Thr	Thr	Asn	Pro		Phe
310					645					650					655	
312	Val	Arg	Cys	Ile	Ile	Pro	Asn	Asn	Lys	Gln	Leu	Pro	Ala	Lys	Leu	Glu
313				660					665					670		
315	Asp	Lys	Val	Val	Leu	Asp	Gln	Leu	Arg	Cys	Asn	Gly	Val	Leu	Glu	Gly
316			675					680				_	685			•
318	Ile	Arq	Ile	Thr	Arg	Lys	Gly	Phe	Pro	Asn	Ara	Ile	Ile	Tvr	Ala	Asp
319		690				-	695				,	700		- 1		
321	Phe	Val	Lvs	Ara	Tyr	Tvr	Leu	Leu	Ala	Pro	Asn		Pro	Δrσ	Agn	Δla
	705		_1 -	5	-1-	710					715		110	1119	nsp	720
		Asp	Ser	Gln	Lys		Thr	Δen	Δla	Va 1		Tare	uic	LOU	λan	
325		F		0211	725	1114		nop.	2114	730	пси	цуз	1113	пец	735	116
		Dro	Glu	Gln	Tyr	λνα	Dho	C1.	т10		T ***	т1.	nha	Dh a		3.1
328	nsp	FIU	Giu	740	тут	AIG	PIIE	GIY		1111	LYS	ire	Pile		Arg	Ата
	G1	01 -	T		3	-1 -	a 1	a 1	745	_	~ 1		_	750		
	СТУ	GIII		Ата	Arg	тте	GIU		АТа	Arg	GLu	GIn	_	Leu	Gly	Ser
331			755					760					765			
	GLu		Thr	Lys	Ser	Asp	Tyr	Leu	Lys	Arg	Ala	Asn	Glu	Leu	Val	Gln
334		770					775					780				
		Ile	Asn	Asp	Lys	Gln	Ala	Ser	Leu	Glu	Ser	Arg	Asp	Phe	Gly	Asp
	785					790					795					800
339	Ser	Ile	Glu	Ser	Val	Gln	Ser	Phe	Met	Asn	Ala	His	Lys	Glu	Tyr	Lys
340					805					810			_		815	-
342	Lys	Thr	Glu	Lys	Pro	Pro	Lvs	Glv	Gln	Glu	Val	Ser	Glu	Leu	Glu	Ala
343	-			820			_		825					830	0_0	
	Tle	Tvr	Asn		Leu	Gln	Thr	T.ve		Δrα	T.011	Tla	Luc		Glu.	Dro
346		-1-	835			01		840	LCu	nrg	Lea	116	845	AIG	GIU	PIO
	Dho	V≥1		Dro	λla	C1++	Lon		Dro	7 ~~	C1	т1 -		0	m1	(II) was to
349	r 11G		чта	FIO	Ala	ату		TIIT	PLO	ASII	GIU		ASP	ser	Tur	Trp
	C ~ ~	850	T a	C1	T	31 -	855	a1 ·	61			860		_	_	
		Ата	ьeu	GLU	Lys		GIU	GID	GLU	HIS		Glu	Ala	Leu	Arg	
	865	_	_	_		870			_		875					880
	GLu	Leu	Ĺys	Arg	Gln	Lys	Lys	Ile	Ala	Val	Leu	Leu	Gln	Lys	Tyr	Asn
355					885					890					895	
357	Arg	Ile	Leu	Lys	Lys	Leu	Glu	Asn	Trp	Ala	Thr	Thr	Lys	Ser	Val	Tyr



Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 04/18/2002

PATENT APPLICATION: US/10/044,303

TIME: 11:06:16

Input Set : A:\Vectorsl.app

Output Set: N:\CRF3\04182002\J044303.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:424 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3 L:424 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3

L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3